

FIGURE 1

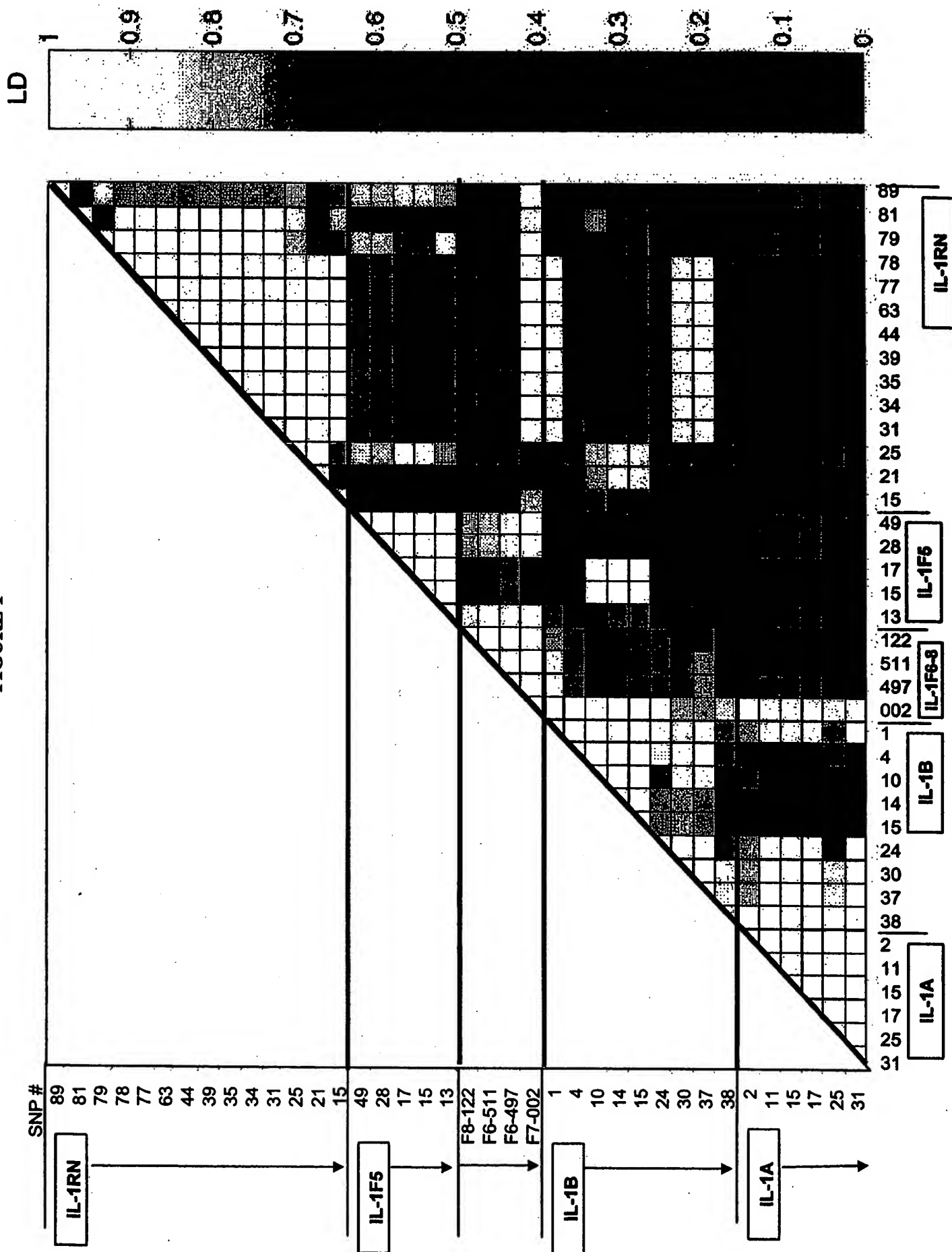


Figure 2A Linkage Disequilibrium (D') Values and their Statistical Significance among representative SNPs of the IL-1 Gene Cluster

SNPs	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	1																			
2		1																		
3			1																	
4				1																
5					1															
6						1														
7							1													
8								1												
9									1											
10										1										
11											1									
12												1								
13													1							
14														1						
15															1					
16																1				
17																	1			
18																		1		
19																			1	
20																				1
21																				
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39																				

Note: Numbers above the diagonal represent $1 - p$ (where p = significance of the Chi-square) values. Numbers below the diagonal represent D' values.

FIGURE 2 A

Figure 2B Linkage Disequilibrium (D') Values and their Statistical Significance among representative SNPs of the IL-1 Gene Cluster																				
SNPs	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	
1	0.3475	0.3584	0.6609	0.6957	0.0502	0.3759	0.2999	0.3054	0.2863	0.2829	0.2903	0.2642	0.2572	0.2592	0.2566	0.6685	0.0718	0.5657	0.5741	
2	0.1404	0.1535	0.1861	0.2174	0.0036	0.3596	0.7162	0.3923	0.4023	0.407	0.4233	0.4148	0.3988	0.4351	0.4472	0.2321	0.1028	0.1222	0.1267	
3	0.3619	0.3739	0.6622	0.6908	0.0197	0.3465	0.3617	0.2965	0.2767	0.2732	0.2806	0.2604	0.2509	0.2493	0.2416	0.6605	0.085	0.6043	0.6119	
4	0.408	0.4218	0.6569	0.6861	0.0281	0.382	0.3914	0.3128	0.2914	0.2875	0.2955	0.2739	0.2636	0.2618	0.2488	0.6543	0.1009	0.5979	0.6057	
5	0.3475	0.3584	0.6609	0.6957	0.0502	0.3759	0.2999	0.3054	0.2863	0.2829	0.2903	0.2642	0.2572	0.2592	0.2566	0.6685	0.0718	0.5657	0.5741	
6	0.0694	0.1112	0.1442	0.1497	0.0139	0.4913	0.4567	0.2589	0.2418	0.2177	0.2436	0.2213	0.1768	0.1433	0.1038	0.0322	0.1767	0.1226	0.1324	
7	0.1374	0.1604	0.2201	0.2481	0.0086	0.3901	0.6124	0.465	0.4734	0.4772	0.4802	0.4935	0.4695	0.4998	0.5054	0.2557	0.0879	0.1537	0.1574	
8	0.0511	0.0695	0.3696	0.3911	0.077	0.3061	0.6649	0.8908	0.892	0.892	0.8929	0.8876	0.8873	0.8979	0.8992	0.3612	0.0597	0.2698	0.289	
9	0.0534	0.075	0.396	0.4156	0.0657	0.3139	0.6442	0.8931	0.8945	0.8952	0.896	0.8912	0.8909	0.9007	0.901	0.3916	0.0693	0.2932	0.2992	
10	0.0205	0.0579	0.415	0.4338	0.0961	0.2094	0.6239	0.8356	0.379	0.3409	0.3021	0.3439	0.2747	0.2158	0.2003	0.2157	0.2429	0.2128	0.273	
11	1	1	0.5326	0.5824	0.5656	0.8676	0.8447	0.6411	0.6057	0.5956	0.5816	0.5655	0.5841	0.5798	0.5901	0.6923	0.6377	0.4049	0.4459	
12	1	1	0.5356	0.5853	0.5683	0.8669	0.8465	0.6391	0.6035	0.5934	0.5793	0.5632	0.5818	0.5775	0.5878	0.6446	0.641	0.4048	0.4463	
13	1	1	0.4785	0.5346	0.7152	0.769	0.8137	0.5437	0.5398	0.5398	0.5319	0.518	0.5518	0.558	0.5557	0.555	0.7765	0.2871	0.3202	
14	0.1953	0.17	0.0947	0.1148	0.3034	0.1834	0.6785	0.6419	0.6038	0.574	0.551	0.5331	0.5651	0.5255	0.5597	0.1164	0.4983	0.0587	0.0052	
15	0.1991	0.2258	0.2963	0.3271	0.0244	0.3521	0.6167	0.8784	0.8818	0.8822	0.8825	0.8747	0.8757	0.8944	0.8891	0.3124	0.0318	0.3114	0.2696	
16	0.07	0.1141	1	1	0.8263	0.2531	0.0164	1	1	1	1	1	1	1	1	1	0.8726	1	1	
17	0.6779	0.6775	0.8441	0.8514	0.2268	0.4428	0.6256	0.6544	0.6883	0.6924	0.6763	0.5932	0.628	0.6034	0.5978	0.3968	0.2508	0.4331	0.425	
18	0.5665	0.5657	0.8181	0.8266	0.242	0.341	0.6467	0.5441	0.5887	0.5933	0.5729	0.5932	0.5391	0.51	0.5018	0.369	0.25	0.4156	0.4066	
19	0.5499	0.5554	0.801	0.8095	0.0964	0.4239	0.6028	0.6144	0.6467	0.6318	0.6318	0.5628	0.5962	0.573	0.5669	0.3527	0.2907	0.3699	0.3689	
20	1	1	1	1	0.1731	0.4708	0.7597	0.5849	0.6038	0.6115	0.6028	0.569	0.5868	0.5913	0.584	0.9344	0.1041	0.7722	0.8022	
21	1	1	1	1	0.409	0.0342	1	0.1186	0.1863	0.1639	0.1804	0.1732	0.2058	0.2625	0.2301	0.6962	0.3323	0.8836	0.8756	
22	1	1	1	1	0.3903	0.0305	1	0.0936	0.1111	0.0704	0.0894	0.0771	0.1224	0.1837	0.1467	0.7023	0.3066	0.8853	0.8781	
23	1	1	1	1	0.424	0.3041	0.8146	0.6153	0.6383	0.6437	0.6372	0.5882	0.606	0.6036	0.6026	0.8187	0.0187	0.8162	0.8358	
24	1	1	1	1	0.4026	0.3333	0.8303	0.6562	0.675	0.6799	0.6745	0.6227	0.6391	0.6437	0.6421	0.8338	0.0078	0.8344	0.8496	
25	0.978	0.952	0.999	0.984	0.841	0.3062	0.7033	1	1	1	1	1	1	1	1	0.5969	0.8335	0.7108	0.7028	
26	0.227	0.166	0.958	0.984	0.997	0.972	1	1	1	1	1	1	0.892	0.8873	0.8859	0.8176	0.8652	0.8072	0.7888	
27	0.984	0.983	1	1	0.997	1	1	1	1	1	1	1	1	0.9814	1	1	1	0.7218	0.7877	
28	0.257	0.202	1	1	1	1	1	1	1	1	1	1	1	0.9821	1	1	1	0.7392	0.8015	
29	0.403	0.206	1	1	1	1	0.999	1	1	1	1	1	1	0.9824	1	1	1	0.7422	0.8015	
30	0.338	0.187	1	1	1	1	0.999	1	1	1	1	1	1	0.982	1	1	1	0.741	0.8004	
31	0.356	0.211	1	1	1	1	0.999	1	1	1	1	1	0.982	0.9641	0.9811	0.9356	1	0.725	0.7872	
32	0.377	0.165	0.998	1	1	1	0.999	1	1	1	1	1	0.982	0.9641	0.9811	0.9356	1	0.725	0.7872	
33	0.398	0.297	1	1	1	1	0.997	0.997	1	1	1	1	1	1	1	1	1	0.7393	0.7993	
34	0.552	0.414	0.999	1	1	1	0.999	0.994	1	1	1	1	1	1	1	1	1	0.7463	0.805	
35	0.456	0.307	1	1	1	1	1	0.995	1	1	1	1	1	1	1	1	1	0.7456	0.8038	
36	0.979	0.978	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.8721	0.9064	
37	0.825	0.788	0.069	0.003	1	0.975	1	1	1	1	1	1	1	1	1	0.152	0.0942	0.0737	0.0942	
38	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.506	0.9662	0.9662	
39	0.997	0.998	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.598	1	1	

Note: Numbers above the diagonal represent 1 - p (where p = significance of the Chi-square) values. Numbers below the diagonal represent D' values.

FIGURE 2 B

GTC Loc		3872	5428	5711	8093	12412	2251	3763	4543	6493	6742	6953	7156	9239	18726	18792	20097	20311	20418	20579	21822
Figure 3B: Organization of specific nucleotides on IL-1 haplotypes: Pattern 1) TTC = 2, 2, 1																					
ILGN SNPs	7	←	←	←	←	←	←	←	←	←	←	←	←	←	←	←	←	←	←	←	←
HAP TAGS	Haptag																				
GTC SNP #	S122	IL13	IL15	IL17	IL128	IL149	RA15	RA21	RA25	RA31	RA34	RA35	RA39	RA44	RA61	RA63	RA77	RA78	RA79	RA81	RA89
	9.25391 C	C	T	A	C	T	T	C	C	G	A	G	T	A	T	G	T	A	T	A	→ C
	3.0703 C	T	T	A	T	C	G	C	C	G	A	G	T	A	T	G	T	A	A	G	T
	1.81561 C	C	C	G	T	C	G	C	C	G	A	G	T	A	T	G	T	A	A	G	T
	1.23456 G	C	T	A	C	T	G	C	T	G	A	G	T	A	T	G	T	A	T	G	C
	0.65352 G	C	T	A	C	T	T	C	T	G	A	G	T	A	T	G	T	A	T	G	C
	0.63874 C	C	T	A	C	T	G	C	C	G	A	G	T	A	T	G	T	A	A	G	T
	0.61728 C	T	T	A	T	C	T	C	C	C	C	A	T	C	T	A	C	T	A	A	T
	0.61728 C	C	T	A	C	T	T	T	C	G	A	G	T	A	C	G	T	A	T	A	C
	0.30864 C	T	C	G	T	C	G	C	C	G	A	G	T	A	C	G	T	A	T	A	C
	0.30864 C	T	C	G	T	C	G	C	C	G	A	G	T	A	C	G	T	A	T	G	T
	0.30864 C	C	T	A	T	C	G	C	C	G	A	G	T	A	C	G	T	A	T	G	T
	19.75304	C	T	A	T	C	G	C	C	G	A	G	T	A	C	G	T	A	A	G	T

FIGURE 3 B

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Figure 4B: Organization of specific nucleotides on IL-1 haplotypes: Pattern 2) GCT = 1 1 2																					
GTC Loc.	7	3872	5428	5711	8093	12412	2251	3763	4543	6493	6742	6953	7156	9239	18726	18792	20097	20311	20418	20579	21822
ILGN SNPs																					
HAP TAGS																					
GTC SNP Freq.	S122	ILL13	ILL15	ILL17	ILL28	ILL49	Haplog RA15	RA21	RA25	RA31	RA34	RA35	RA39	RA44	RA61	RA63	RA77	RA78	RA79	Haplog RA81	RA89
8.13959	C	T	T	A	T	C	T	C	C	C	C	A	C	C	C	A	C	T	A	A	T.
2.85817	C	T	A	A	T	C	G	C	C	G	A	G	T	A	T	G	T	A	A	G	T.
1.73695	C	T	A	A	T	C	T	C	C	C	C	A	C	C	C	A	C	T	A	A	C
1.34788	C	T	A	A	T	C	T	C	C	C	C	A	C	C	C	A	C	T	A	A	C
1.23456	G	C	T	A	C	T	T	C	T	G	A	G	T	A	T	G	T	A	T	G	C
1.23456	C	T	A	A	T	C	T	C	C	C	C	A	C	C	C	A	C	T	A	A	T
0.73221	C	C	G	G	T	C	T	C	C	C	C	A	C	C	C	A	C	T	A	A	T
0.61728	C	T	A	A	T	C	G	C	G	A	G	G	T	A	T	G	T	A	A	A	T
0.61728	G	C	G	G	T	C	T	T	C	C	C	A	C	C	T	G	T	A	A	G	T
0.61728	C	T	A	A	T	C	G	C	C	G	A	G	T	A	T	G	T	A	A	A	T
0.61728	C	T	A	A	C	T	T	C	C	C	C	A	C	C	C	A	C	T	A	A	T
0.61728	C	T	A	A	T	C	T	C	C	C	C	A	C	C	C	A	C	T	A	A	C
0.61728	C	T	A	A	T	C	G	C	C	G	A	G	T	A	T	G	T	A	A	G	T
0.61728	G	C	A	A	C	T	T	C	C	C	C	A	C	C	C	A	C	T	A	A	T
0.61728	C	T	A	A	T	C	T	C	C	C	C	A	C	C	C	A	C	T	A	A	T
0.41686	C	T	A	A	T	C	T	T	C	G	A	G	T	A	C	G	T	A	A	A	C
0.30864	C	T	A	A	T	C	T	C	C	G	A	G	T	A	C	G	T	A	A	G	T
0.30864	C	T	A	A	T	C	T	C	C	G	A	G	T	A	C	G	T	A	A	A	T
0.20041	C	T	A	A	T	C	T	T	C	G	A	G	T	A	C	G	T	A	T	A	C

Figure 5A: Organization of specific nucleotides on IL-1 haplotypes: Pattern 3) GCC = 1 1 1

Details on the haplotypes derived from the Sheffield families, in relation to the ILGN functional and GTC SNPs - 38 sites used in the LD map

GTC Loc	15191	11079	10963	8099	6483	5342	4725	2467	14233	13921	12561	10965	10888	6970	6490	5521	3243	18247	7	7
ILGN SNPs																				
HAP TAGS																				
GTC SNP Freq																				
IL31	IL26	IL25	IL17	IL15	IL11	IL12	Haptag	IL38	IL37	IL30	IL25	IL24	IL15	IL14	IL10	IL4	IL1	S02	S497	S511
7.98845 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	A	T
4.91681 A	G	T	A	T	C	C		T	G	G		A	T		G	T	T	C	A	T
3.7037 C	G	T	C	A	T	T		T	G	G		G	T		G	T	T	C	G	T
3.08641 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
2.58406 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
2.3423 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
2.24088 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
1.85185 C	T	T	C	A	T	T		T	G	G		A	T		G	T	T	C	A	T
1.38412 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
1.23456 C	T	T	C	A	T	T		T	G	G		A	T		G	T	T	C	G	C
1.23456 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
1.23456 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
0.63339 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
0.62263 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
0.61728 C	T	T	C	A	T	T		T	G	G		A	T		G	T	T	C	G	C
0.61728 C	T	T	C	A	T	T		T	G	G		A	T		G	T	T	C	G	C
0.61728 C	T	T	C	A	T	T		T	G	G		A	T		G	T	T	C	G	C
0.61728 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
0.61728 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
0.61728 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
0.1149 A	T	T	A	T	C	C		T	G	G		A	T		G	T	T	C	G	C
0.07716 C	T	T	C	A	T	T		T	G	G		A	T		G	T	T	C	G	C
0.07716 C	T	T	C	A	T	T		T	G	G		A	T		G	T	T	C	G	C
0.07716 C	T	T	C	A	T	T														

FIGURE 5 A

[illegible]

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List of SNPs not included in the LD table and diagram of LD and/or HAP blocks. These SNPs are in strong LD with one or more of the SNPs included in the LD table.

Gene	GTC SNP/Site #*	Combination of sites with > 0.9 LD
IL-1A	1	1 and 2
	3	2 and 3
	5	4 and 5
	10	9 and 10
	12	11 and 12
	14	13 and 14
	16	15 and 16
	19	18 and 19
	26	25 and 26
	32	31 and 32
	34	33 and 34
IL-1B	2	1 and 2
	3	3 and 4
	5	4 and 5
	6	5 and 6
	7	6 and 7
	8	7 and 8
	9	8 and 9
	17	High heterozygosity and Informative
IL-1F5	5	5 and 6
	7	6 and 7
	9	8 and 9
	10	9 and 10
	11	10 and 11
	14	13 and 14
	22	21 and 22
	23	22 and 23
	24	23 and 24
	27	27 and 28
	29	28 and 29
	35	High heterozygosity and Informative
	36	36 and 37
	38	High heterozygosity and Informative
	40	High heterozygosity and Informative
	43	High heterozygosity and Informative
	45	High heterozygosity and Informative
	48	47 and 48
	50	49 and 50
	51	High heterozygosity and Informative
	54	54 and 55
	56	55 and 56
	57	56 and 57

FIGURE 7 A

Gene	GTC SNP/Site #	C mbInation f sites with > 0.9 LD
IL-1RN	14	14 and 15
	19	High heterozygosity and Inf rnative
	22	21 and 22
	30	30 and 31
	36	35 and 36
	37	High heterozygosity and Informative
	38	37 and 38
	40	39 and 40
	43	43 and 44
	62	62 and 63
	64	High heterozygosity and Informative
	76	76 and 77
	82	81 and 82

* Note: Numbers in this column represent the position of SNPs in the GTC sequence panel, consisting four genes. For example, in the gene IL1-A, sites # 1, 3 and 5 correspond, respectively, to SNP sites 2346, 2505 and 3116 in the GTC map.

FIGURE 7 B

IL-1 α

SNP #	GTC Location	Base # in IL-1 α gene	Relative to +1	Region	cdN A	Location	AA#	Mutation	Type	%	SNP Sequence
1	2346	1553	-3885	343903		Promoter			C/T	C=98% T=2%	GCATGAGCCACGCGACCCAGCCACT
2	2467	1674	-3764	343782		Promoter			C/T	C=62 T=38	TGAACCTAGAACTCAAGAAATTGA
3	2505	1712	-3726	343744		Promoter			T/C	T=98 T=2	CACACTCTCATATGAATTCCTCAT
4	2623	1830	-3608	343626		Promoter			G/A	G=62 A=38	CATATCTGGGACCTTCAATAAA
5	3116	2323	-3115	343133		Promoter			C/T	T=74 C=26	AAAAGTATGTTTTCTCTTCATCA
6	3475	2682	-2756	342774		Promoter			C/T	C=66 T=34	TCCTTATAAGCCATCATTGGTG
9	3962	3169	-2269	342287		Promoter			G/A	G=70 A=30	CGAGAGGTGGTGCTGCTGAAGCCACC
10	4113	3320	-2118	342136		Promoter			C/T	C=98 T=2	TGTTACAGTCCAGAAAAGCGGC
11	4725	3932	-1506	341504		Promoter			C/T	C=68 T=32	TAAAGAGGAAACCAAGGTAAAGCAGAA
12	5029	4236	-1202	341220		Promoter			C/T	C=78 T=22	ACACAAGCTGCTTTCTCCOCAGATC
13	5342	4549	-889	340907		Promoter			C/T	C=72 T=28	CCAGGCAACACCATTTGAAGGCTC
14	6377	5583	+145	340907		Intron 1			C/T	C=78 T=22	AAAGCTACAGCCTCTCTTCTTT
15	6483	5689	+251	339766		Intron 1			T/A	T=66 A=34	CTGATTCGTTTACTGAGGGACG
16	6495	5701	+263	339754		Intron 1			G/A	G=70 A=30	ACTGAGGGACGCGCAGAACTAGTTTC
17	8099	7302	+1864	338150		Intron 3			A/C	A=66 C=34	CTTGAATCTTAAATACITTTTGT
18	8127	7330	+1892	338122		Intron 3			G/A	G=72 A=28	CTCACTAGAGTCCAGAGACCT
19	9058	8260	+2822	337191	290	Exon 4	85	R to Q	G/A	G=98 A=2	AAGAAGAGACGGTTGAGTTT
24	10950	10153	+4718	335286		Intron 4			A/C	A=78 C=22	TCTGGATTGGAATATTCCTA
25	10963	10166	+4728	335286		Intron 4			T/C	T=72 C=28	ATTCTAATAITCCCTCCAG
26	11079	10282	+4845	335170	376	Exon 5	114	A to S	G/T	G=72 T=28	GCCTAGGTCAAGCACTTTTAG
30	12864	12065	+6627	333385		Intron 6			G/C/ A	G=38 C=36 A=26	GCCCCACCTNGCCACCCCA
31	15191	14249	+8811	331038		Intron 6			A/C	A=68 T=32	CCTTTTCTAACATCTTGTCTCTA
32	15840	14898	+9460	330409	1260	Exon 7 3' UTR			G/A	A=74 G=26	TTTGCCTTCTACTTTTAAGTT
33	15993	15051	+9613	330256	1440	Exon 7 3' UTR			C/T	T=72 C=28	AAATACTTCTTNGAAGCCGAGC
34	16129	15187	+9749	330120	1549	Exon 7 3' UTR			C/G	C=96 G=4	CTGAGTGTGA\CCAGGCATCCTC

FIGURE 8

IL-1 β

SNP#	GTC Location	Base # in IL-1 β gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence
1	1824	770	-5164	397483		Promoter			C/T	C=84 T=16	GCCTGGGTCCICAGACTTGACAAA
2	3029	1975	-3959	396278		Promoter			T/C	T=96 C=4	AGAAAAGACATAGAGTAGGA
3	3095	2041	-3893	396212		Promoter			G/A	G=70 A=30	TCCAAAGGAAIGGACAAAGTC
4	3243	2189	-3745 (-3737)	396063		Promoter			C/T	C=62 T=38	GGGAGGAGAAATGGAATGTCCCTTGGACTCT
5	3302	2248	-3686	396005		Promoter			A/G	A=98 G=2	GAAGAAGCCCAATTGGAGATGATG
6	3734	2680	-3254	395573		Promoter			T/C	T=96 C=4	GATAACTGGCTTGCAGAGCCCATGAT
7	4083	3029	-2905	395224		Promoter			A/G	A=98 G=2	GGAAGACAGGATCTGTATACATAC
8	4594	3540	-2394	394713		Promoter			G/A	G=98 A=2	CCTGTCACTGGCTTTTGATCCTCCTT
9	4610	3556	-2378	394697		Promoter			G/A	G=96 A=4	ATCCTCCTTCGTTTCAGCTTGTATC
10	5521	4464	-1470 (-1464)	393786		Promoter			G/C	G=70 C=30	CACTCCTTGTGATAATGCAGAGGGAG
14	6490	5423	-511	392837		Promoter			T/C	T=54 C=46	AGAGAGCTCCTTGAGGCAGAGAAC
15	6970	5903	-31	392337		Promoter			C/T	C=54 T=46	TTTTGAAAAGCICATAAAAAACAGCGAGGGAG
17	7046	5979	+45	392261	45	Exon 1 5' UTR			T/C	T=54 C=46	GCTCTGGGATTCCTCTTCAGCCAATCTTCAT
19	7750	6680	+746	391557		Intron 2			C/T	none	ACTACTTTCCCAATTACAAAGTCCCTCCAG
24	10888	9810	+3876	388419		Intron 4			G/A	G=64 A=36	AAATTTTGGCGCTCGCCCTCAGGAG
25	10965	9887	3953	388342	401	Exon 5	105	F to F	T/C	C=78 T=22	CTATCTTCTTCGACACATGGGATAACG
30	12561	11482	+5548	386746		Intron 6			G/A	G=78 A=22	CCCTTCTCCCGGCCCCCATCCCTAGG
35	13517	12440	+6506	385790	997	Exon 7 3' UTR			C/A	C=98 A=2	ATAGCCTGGAICTTTCCTGTGTCT
37	13921	12845	+6911	385386	1401	Exon 7 3' UTR			G/C	G=78 A=22	CTTTAATTAAAGACTGAAAATATATAAGC
38	14233	13148	+7214	385074					C/T	C=84 T=16	CAGTGCACATCTTGGAAACAGGATC

FIGURE 9

IL-1 RNic

SNP#	GTC Location	Base # in IL-1 RN Gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence
14	2189	11268	-4864	669240					G/A	G=86 A=14	GTTGGGTCACTACCCGACGTGCTA
15	2251	11330	-4744	669277					T/G	T=76 G=24	ACTGTTACATAGCCAAAGATATGGA
18	3332	12412	-3662	670358					T/G	T=56 G=4	TGTTTGCTGTTCTCTCTCTCAGC
19	3576	12657	-3417	670602					A/G	G=80 A=20	AGCTGGGTCTGTGAGTTGTGTGGC
21	3763	12844	-3230	670789					C/T	C=82 T=18	GTGTGTGTGCTGTGTGTGTGTG
22	3803	12886	-3188	670829					G/A	G=98 A=2	GAGAGAATGAAGAATATGAGTGTGG
25	4543	13626	-2448	671580					T/C	C=78 T=22	TATCTTGCTCTCTCCATTCTCTGATC
26	4648	13731	-2343	671674					T/C	T=98 C=2	GTCAACATCAATTGGGGTTGTGGATC
29	5534	14616		672560		Promoter			C/T	C=98 T=2	TGAGCCAAAGTCGGAAGAGAAACAGGA
30	5992	15073	-1002	673020		Promoter			T/C	T=74 C=26	GCAGATAGCAATCAGGTCCATTITGC
31	6493	15573	-501	673519		Promoter			G/C	G=70 C=30	CTCTCAGAGA\GGGCTTCCCTGGGCA
32	6494	15574	-500	673520		Promoter			G/A	G=98 A=2	TCTCAGAGAGGGCTTCCCTGGGCAC
33	6606	15686	-388	673632		Promoter			C/T	C=70 T=30	TATTTATTGCTAACTTGTTCITG
34	6742	15822	-252	673768		Promoter			A/C	A=70 C=30	GCACACATGCATGAGCTGGCGGCAG
35	6953	16033	-41	673979		Promoter			G/A	G=70 A=30	GGGAGGGGAG\GCTGGGCTCCTCCTT
36	7034	16114	+40	674060	36	Exon 1 5' UTR			G/A	G=70 A=30	CCCAGGTACTGCGCGGGGTGCTACTT
37	7090	16170	+96	674116	92	Exon 1 5' UTR			G/A	G=74 A=26	GGAAGACCTCGGAAGAGACCCTCTGTC
38	7109	16189	+115	674135	111	Exon 1 5' UTR			G/C	G=70 C=30	CCTGTCTATGAGGCCCTCCCATG
39	7156	16235	+162	674182		Intron 1			T/C	T=70 C=30	TCTCAATTTTTCACCTGAGAAATGA
40	7298	16378	+304	674324		Intron 1			A/G	A=70 G=30	GGAGGCATCCATGGGAGACCATGCA
42	9021	18100	+2027	676047		Intron 1			G/T	G=80 T=20	GTGCATACTCGGACTGGAAACTGGA
43	9064	18143	+2060	676090		Intron 1			G/C	G=70 C=30	AAAGGATAGA\GATGGAACCATGTGC
44	9239	18316	+2245	676265		Intron 1			A/C	A=70 C=30	AGGGTAAATTATTTTATAGGATCCAA

FIGURE 10 A

IL-1 RNic (Continued)

SNP#	GTC Location	Base # in IL-1 RN Gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence
61	18726	27810	+11732	685752	239	Exon 3	39	A to A	T/C	T=72 C=28	AAC TAGTTCCTGGATACCTTGCAAGG
62	18781	27865	+11787	685807		Intron 3			T/C	T=74 C=26	GCCAGGAAAGTCAATGTATGTGGGC
63	18792	27876	+11797	685818		Intron 3			G/A	G=72 A=28	CAATGATGNGGGCATCACGTCCT
64	18813	27897	+11819	685839		Intron 3			G/C	G=72 C=28	CAC TTGCCC GTC TGTCTG CAGCAG
65	18841	27938	+11860	685880		Intron 3			T/G	T=88 G=12	TGCACAAACCCCTAGGTCATGTCCTAATC
66	18857	27941	+11855	685903		Intron 3			A/C	A=72 C=28	AAACCC TAGTGC AATGTCCTAATC
67	18892	27975	+11890	685918		Intron 3			T/C	T=96 C=4	TGTATTCAAGTTTGAAGCTGGGAGG
68	18895	27979	+11892	685921		Intron 3			G/A	G=98 C=2	ATTCAA GTTTGAAGCTGGGAGGGCC
76	20075	28987	+13070	687101		Intron 3			G/A	G=74 A=26	AAAAATACCCGGGGGTCTCTTCAITTA
77	20097	29010	+13092	687123		Intron 3			T/C	T=70 C=30	TTATTGCTGCTTCCTCTCTCTATTA
78	20311	29224	+13307	687337		Intron 3			A/T	A=78 T=22	AAACAACCAAAATTTTCTTATGA
79	20418	29331	+13414	687444		Intron 4			T/A	T=58 A=42	GCAGAGTGCCTGGCTTGGCTGGGC
80	20524	29436	+13520	687550		Intron 4			T/G	T=76 G=24	GCATGGGGCTGACTTCCAAAAGGG
81	20579	29491	+13575	687605		Intron 4			G/A	G=50 A=50	CGCTTATTATGACTTCTGCTTGCAT
82	20618	29531	+13614	687644		Intron 4			C/T	C=70 T=30	AAGCCAGTCAICGTGGCTAAGTCTAG
89	21822	30735	+14818	688848	458	Exon 4	112	S to S	T/C	T=60 C=40	GCTCAGACAGTGGCCCCCACCACG

FIGURE 10 B

IL-1 RNsec

SNP#	GTC Location	Base # in IL-1 RN gene	Relative to +1	Region	cDNA	Location	AA#	Mutation	Type	%	SNP Sequence
61	18726	27810	2014 (+2018)	685752	194	Exon 2	57	A to A	T/C	T=72 C=28	AACTAGTTGCTGGATACCTTGCAAGG
62	18781	27865	2069	685807		Intron 2			T/C	T=74 C=26	GCCAGGAAAGTCAATGTATGTGGGC
63	18792	27876	2080	685818		Intron 2			G/A	G=72 A=28	CAATGTATGTGGGCATCAGTCACT
64	18813	27897	2101	685839		Intron 2			G/C	G=72 C=28	CACCTTGCCCGTCTGTCTGCAGCAG
66	18857	27938	2142	685903		Intron 2			A/C	A=72 C=28	AAACCTAGGTGCAATGTCTTAATC
67	18892	27976	2180	685918		Intron 2			T/C	T=96 C=4	TGTATTCAAGTTTGAAGCTGGGAGG
68	18895	27979	2183	685921		Intron 2			G/A	G=98 C=2	ATTCAAGTTTGAAGCTGGGAGGGCC
76	20075	28988	3192	687101		Intron 2			G/A	G=74 A=26	AAAAATACCCGGGGTCTCTTCATTA
77	20097	29010	3214	687123		Intron 2			T/C	T=70 C=30	TTATTGCTGCTTCTCTCTTCTATTAA
78	20311	29224	3428	687337		Intron 2			A/T	A=78 T=22	AAACAACCAAAATTTTCTTATGA
79	20418	29331	3535	687444		Intron 3			T/A	T=58 A=42	GCAGAGTCCCTGGCTTGGCTGGGC
80	20524	29437	3641	687550		Intron 3			T/G	T=76 G=24	GCATGGGGGCTGACTTCCAAAAAGGG
81	20579	29492	3696	687605		Intron 3			G/A	G=50 A=50	CGCTTATTATGACTTCTGCTTGCAAT
82	20618	29531	3735	687644		Intron 3			C/T	C=70 T=30	AAGCCAGTCAICGTGGCTAAGTCTAG
89	21822	30735	4939	688848	413	Exon 4	130	S to S	T/C	T=60 C=40	GCTCAGACAGCGGGCCCCACCACAG
90	22104	31017	5221	689130		Exon 4 3' UTR			C/G	C=60 G=40	GGCGTCACAACAACCTGGTCACAGG
91	22930	31843	6047	689956		Exon 4 3' UTR				insertion	CTCCCCACCAGGCTGGAGCTCTG
93	23062	32206	6410	690319					T/C	T=68 C=32	GCAAAAAAGATATGGGGCAGCACTG
94	23293	32236	6440	690349					A/G	A=98 G=2	AACAGCCTCTACTGGAAACAACCCA
95	23323	31975	6179	690088					A/G	A=96 G=4	AAAGTCCCTACTTCTCTGTGACTTC

FIGURE 11

Cleavage of IL-1 α Variants by Calpain

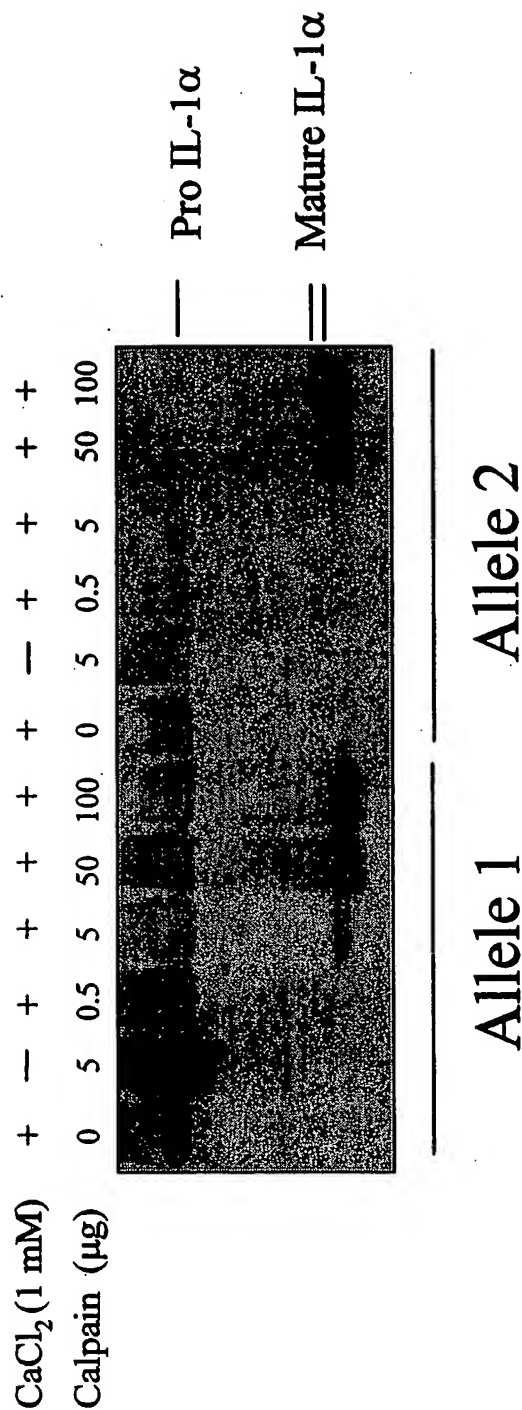


FIGURE 12

Proliferation Rate of Fibroblast Cells Stably Transfected with Allele 1 and Allele 2 of IL-1 α

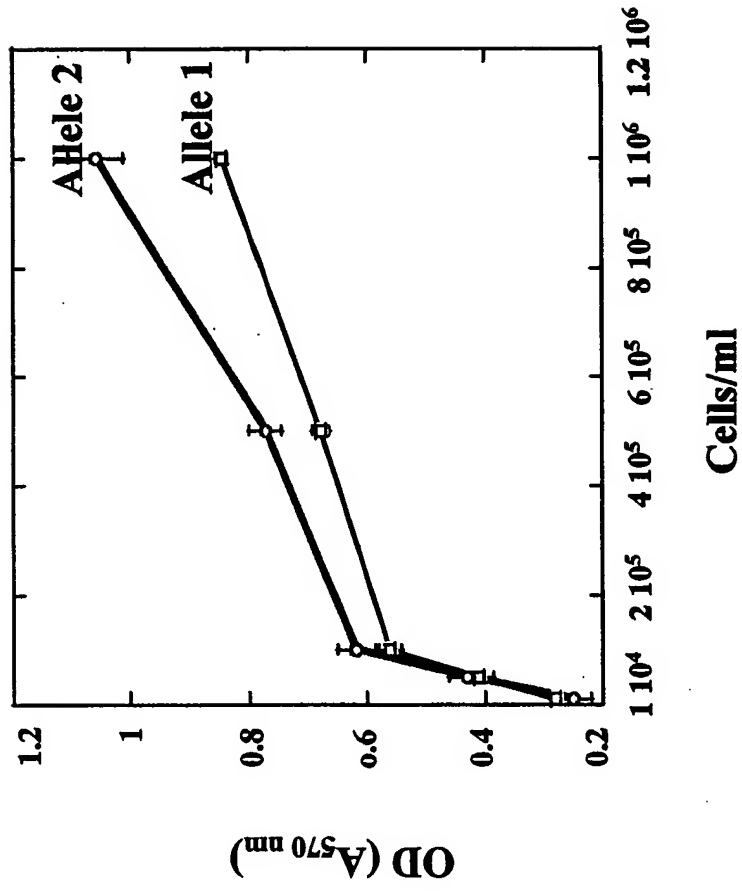
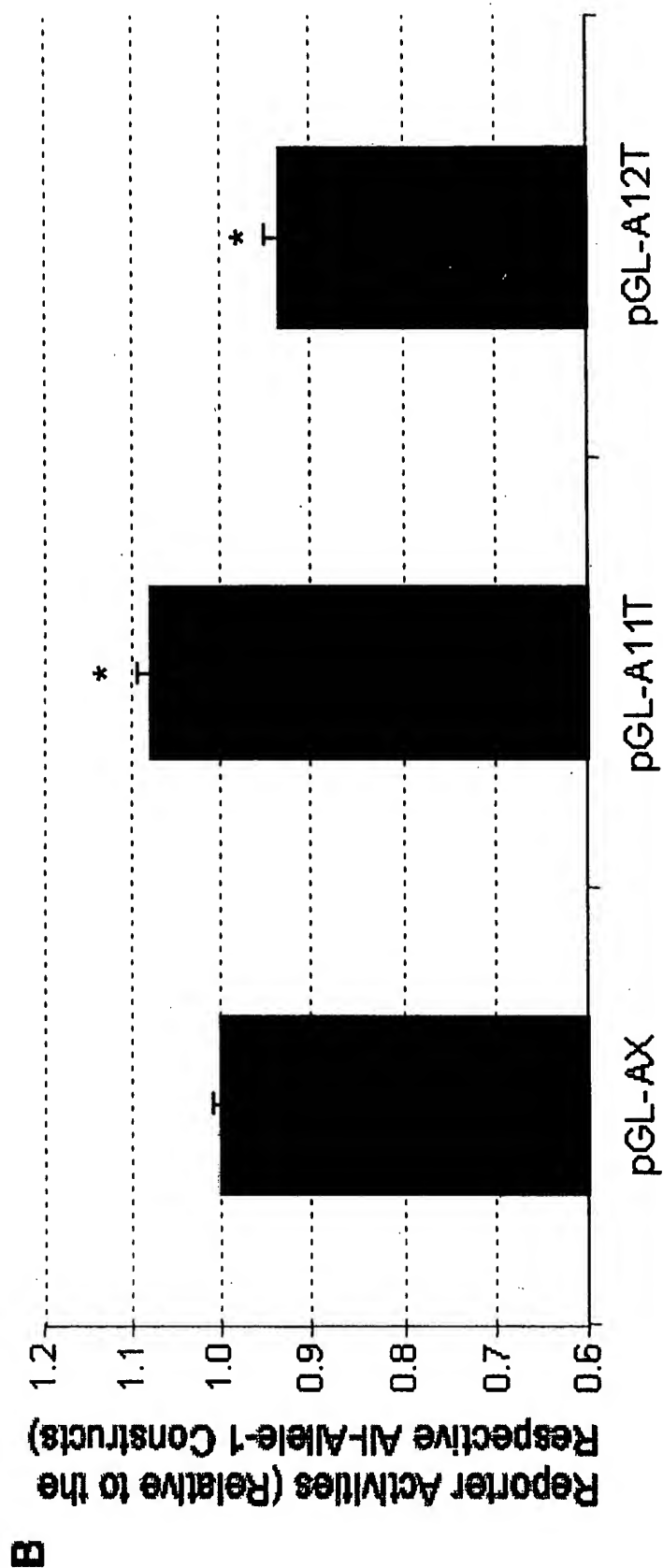
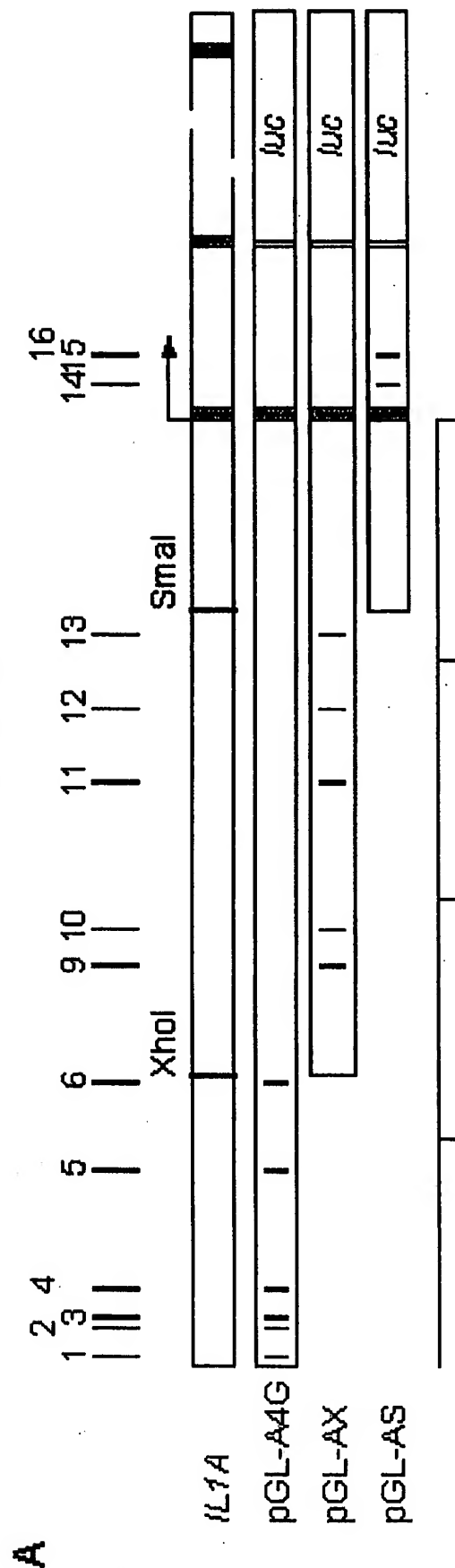


FIGURE 13

IL1A SNP Construct Genotypes

Constructs/SNP#	1	2	3	4	5	6	9	10	11	12	13	14	15	16
pGL-AL4G	C	C	T	G	T	C	G	C	C	C	C	C	T	G
pGL-A1T		C	T	G	T	C	G	C	C	C	C	C	T	G
pGL-A2T	C		T	G	T	C	G	C	C	C	C	C	T	G
pGL-A3C	C	C		G	T	C	G	C	C	C	C	C	T	G
pGL-A4T	C	C	T		T	C	G	C	C	C	C	C	T	G
pGL-A5C	C	C	T	G		C	G	C	C	C	C	C	T	G
pGL-A6T	C	C	T	G	T		G	C	C	C	C	C	T	G
pGL3-IL1AL3X							G	C	C	C	C	C	T	G
pGL-A9A								C	C	C	C	C	T	G
pGL-A10T							G		C	C	C	C	T	G
pGL-A11T							G	C		C	C	C	T	G
pGL-A12T							G	C	C		C	C	T	G
pGL-A13T							G	C	C	C	C	C	T	G
pGL3-IL1AL3SX												C	T	G
pGL-A14T														G
pGL-A15A												C		G
pGL-A16A												C	T	

FIGURE 14 B



IL1A Promoter SNP Constructs

FIGURE 15 A

IL1B SNP Construct Genotypes

Constructs/SNP#	1	2	3	4	5	6	7	8	9	10	14	15	17
pGL3-IL1BS	T	T	G	C	A	T	A	G	G	G	C	T	
pGL-B1C		T	G	C	A	T	A	G	G	G	C	T	
pGL3-IL1BS3KM		T	G	C	A	T	A	G	G	G	C	T	
pGL-B2C		T	G	C	A	T	A	G	G	G	C	T	
pGL-B3A		T	G	C	A	T	A	G	G	G	C	T	
pGL-B4T		T	G	C	A	T	A	G	G	G	C	T	
pGL-B5G		T	G	C	A	T	A	G	G	G	C	T	
pGL-B6C		T	G	C	A	T	A	G	G	G	C	T	
pGL-B7G		T	G	C	A	T	A	G	G	G	C	T	
pGL-B8A		T	G	C	A	T	A	G	G	G	C	T	
pGL-B9A		T	G	C	A	T	A	G	G	G	C	T	
pGL-B10C		T	G	C	A	T	A	G	G	G	C	T	
pGL-B14T		T	G	C	A	T	A	G	G	G	C	T	
pGL-B15C		T	G	C	A	T	A	G	G	G	C	T	
pGL3-IL1BL3KM		T	G	C	A	T	A	G	G	G	C	T	C
pGL-B17T		T	G	C	A	T	A	G	G	G	C	T	

FIGURE 15 B

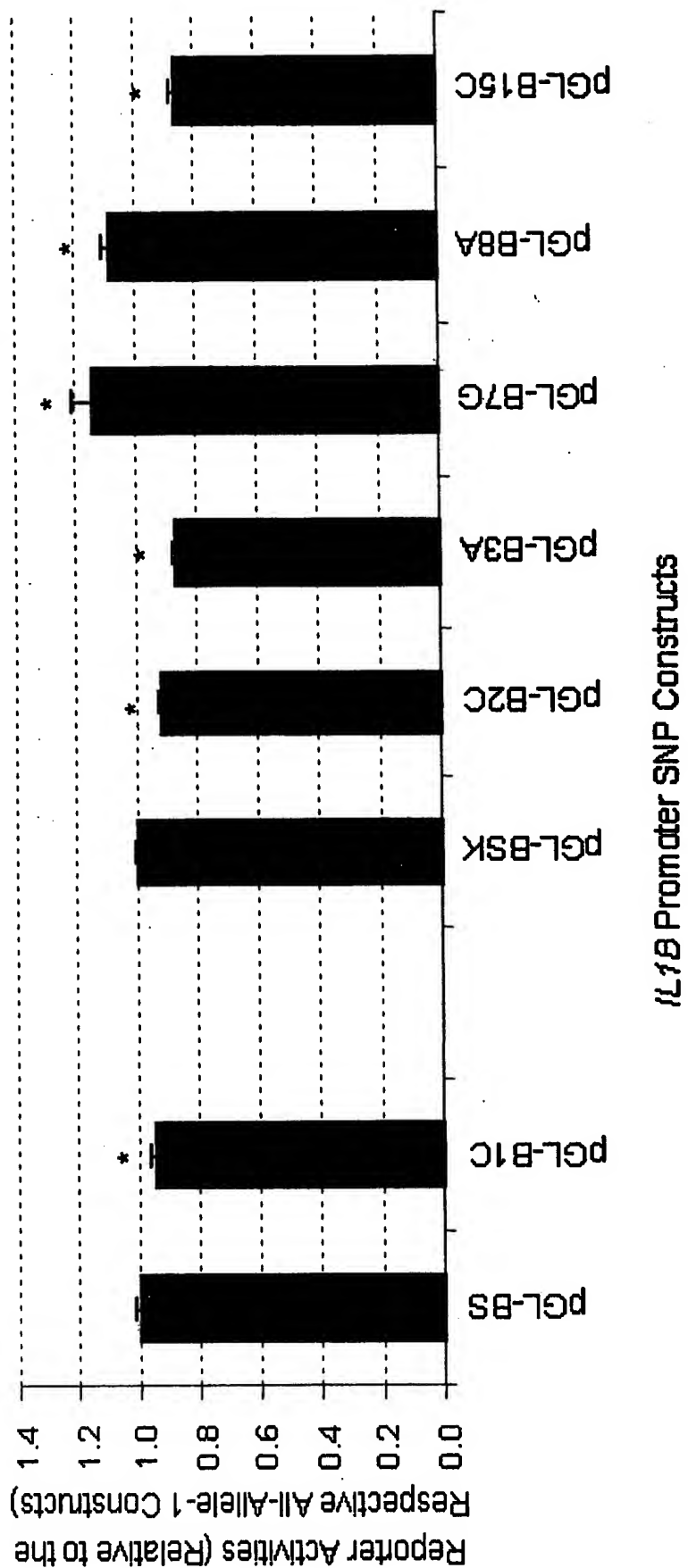
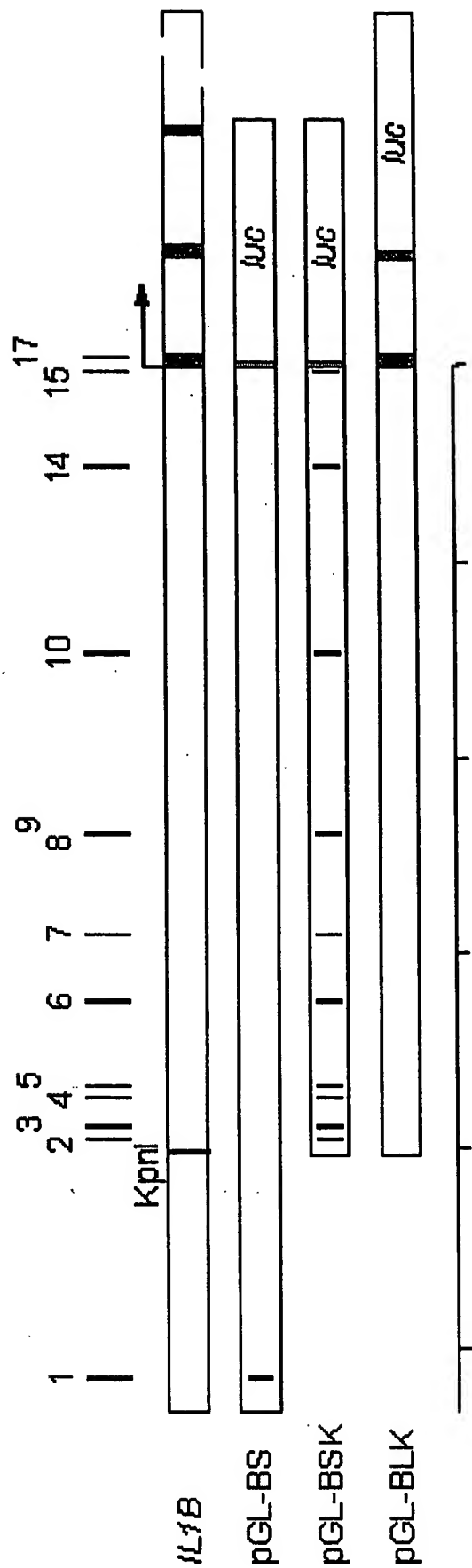
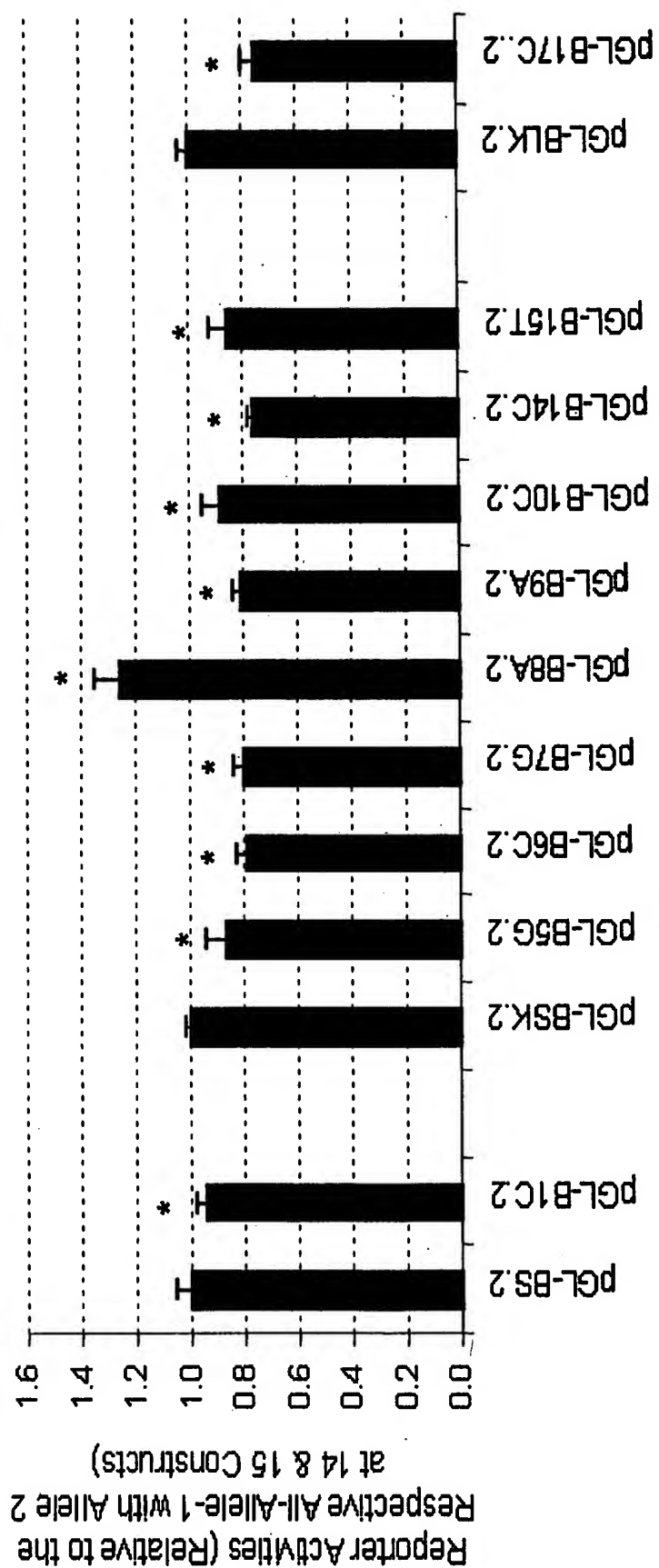
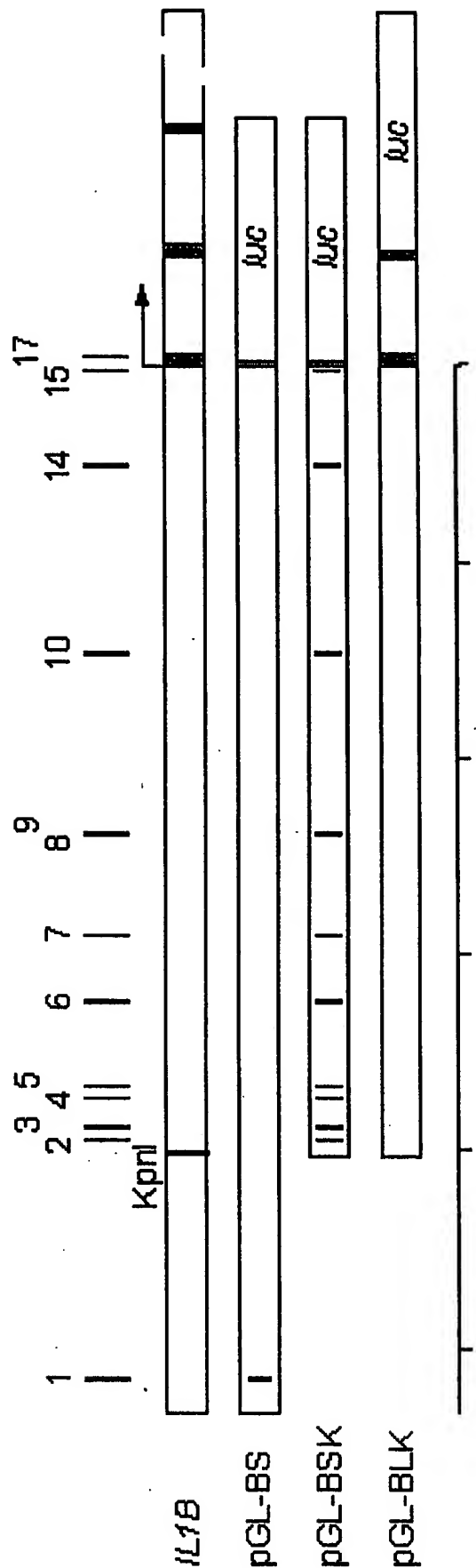


FIGURE 15 C

Constructs	SNP #	1	2	3	4	5	6	7	8	9	10	14	15	17
pGL-B8.2		T	T	G	C	A	T	A	G	G	G	T	C	
pGL-B1C.2		C	T	G	C	A	T	A	G	G	G	T	C	
pGL-B8K.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B2C.2			C	G	C	A	T	A	G	G	G	T	C	
pGL-B3A.2			T	A	C	A	T	A	G	G	G	T	C	
pGL-B4T.2			T	G	T	A	T	A	G	G	G	T	C	
pGL-B5G.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B6C.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B7G.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B8A.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B9A.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B10C.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B14T.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B15C.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-BLK.2			T	G	C	A	T	A	G	G	G	T	C	
pGL-B17T.2			T	G	C	A	T	A	G	G	G	T	C	

FIGURE 15 D



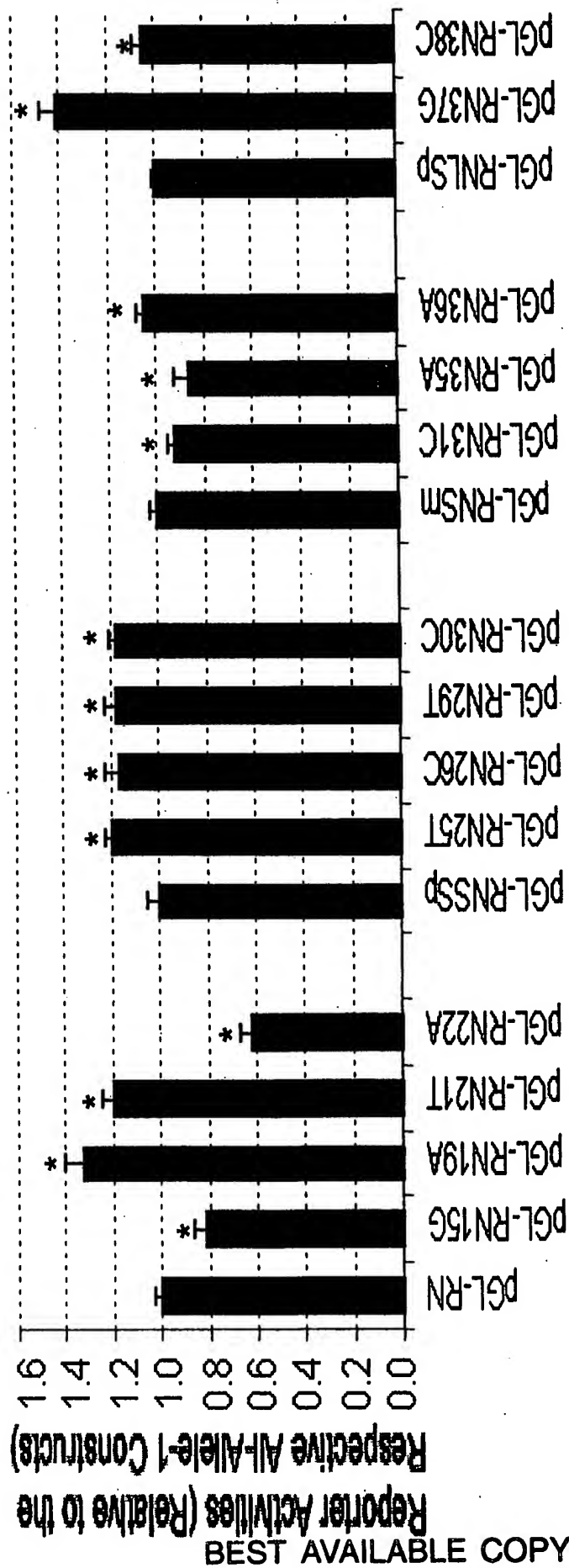
IL-1B Promoter SNP Constructs (Allele 2 at 14 and 15)

FIGURE 16 A

IL1RN SNP Construct Genotypes

Constructs/SNP#	15	18	19	21	22	25	26	29	30	31	32	33	34	35	36	37	38
pGL3-IL1RNS	T	T	G	C	G	C	T	C	T	G	G	C	A	G	G		
pGL-RN15G				C	G	C	T	C	T	G	G	C	A	G	G		
pGL-RN18G	T		G	C	G	C	T	C	T	G	G	C	A	G	G		
pGL-RN19A	T			C	G	C	T	C	T	G	G	C	A	G	G		
pGL-RN21T	T	T	G		G	C	T	C	T	G	G	C	A	G	G		
pGL-RN22A	T	T	G	C		C	T	C	T	G	G	C	A	G	G		
pGL3-IL1RNS						C		C	T	G	G	C	A	G	G		
pGL-RN25T								C	T	G	G	C	A	G	G		
pGL-RN26C						C			T	G	G	C	A	G	G		
pGL-RN29T						C			T	G	G	C	A	G	G		
pGL-RN30C						C			T	G	G	C	A	G	G		
pGL3-IL1RN3S										G	G	C	A	G	G		
pGL-RN31C											G	C	A	G	G		
pGL-RN32A												C	A	G	G		
pGL-RN33T												C	A	G	G		
pGL-RN34C												C	A	G	G		
pGL-RN35A												C	A	G	G		
pGL-RN36A												C	A	G	G		
pGL3-IL1RNL3SX												C	A	G	G	A	G
pGL-RN37G												C	A	G	G	A	G
pGL-RN38C												C	A	G	G	A	G

FIGURE 16 B



icIL1RN Promoter SNP Constructs

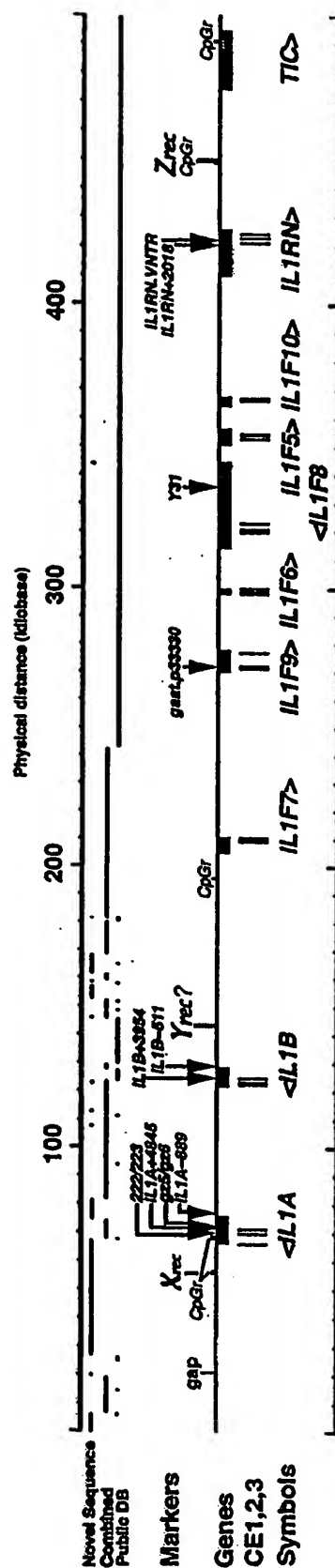


FIGURE 17

Gene: <i>IL1A</i> (<i>IL1F1</i>)		Orientation: Reversed	
Position	Exon	Exon boundaries	Type
065938-067002	IL1A-7	<u>GAGATGCTGAGATA-ACATAATTAACCTTG</u>	CE3 + 3'
069496-069620	IL1A-6	<u>TGAATTTGACATGG-CCAGTGTCTGCTGAAG</u>	CE2
071005-071175	IL1A-5	<u>AAATCATCAAGCCTA-ATCTGGATGAAGCAG</u>	PS + CE1
073111-073333	IL1A-4	<u>AAATCCTTCTATCAT-ATGACTCAGAGGAAG</u>	PS
074223-074271	IL1A-3	<u>TGAATATGAAGAAGA-CTGTCTCTGAATCAG</u>	PS
075233-075287	IL1A-2	<u>AACTCAAGATGGCCA-GAAGAACTGTTACAG</u>	5' + PS
075952-076002	IL1A-1	<u>AACTGCCAGCCAGA-TTTGAGTCAAGCAAG</u>	5'
Coding Interleukin-1α			
cDNA sequence NM_000575, genomic sequence X03833.			
IL1A-1: ∅			
IL1A-2: makvpdmfdef lkncys ²			
IL1A-3: eneedsssid hlsing ³			
IL1A-4: ksfyhvsygp lhgcmdqsv slsisset skltfkemv vvatngkvk krrlslsqsl tdddlealan ⁴			
IL1A-5: iikprsapfs flsnvkynfm riikvefiln dalngsiira ndqyltaaal hnldeav ¹			
IL1A-6: kfdmgaykss kddakitvil risktqlvyt aqdedpvlil k ²			
IL1A-7: empeipktit gsetnllffw ethgtknyft svahpnlfia tkqdywvcla ggppsaitdr qilenga*			

FIGURE 18 A

Gene: <i>IL1B</i> (<i>IL1F2</i>)	Orientation: Reversed	
Position	Exon	Exon boundaries
121295-122108	<i>IL1B-7</i>	<u>AGGTAGATCCCAA-TAACTTCACTGAAG</u>
122827-122957	<i>IL1B-6</i>	<u>TGGTCTCTCCATGT-ACTCTACAGCTGGAG</u>
124196-124360	<i>IL1B-5</i>	<u>AACCTATCTTCTTCG-ATATGGAGCAACAAG</u>
124908-125109	<i>IL1B-4</i>	<u>TGCTCCTCCAGGAC-TCATCTTTGAAGAAG</u>
127099-127150	<i>IL1B-3</i>	<u>TGGCAATGAGGATGA-CCTAAACAGATGAAG</u>
127715-127777	<i>IL1B-2</i>	<u>GTGCTGGAGCAGC-GATGGCTTATTACAG</u>
128240-128311	<i>IL1B-1</i>	<u>ACCAACCTCTTCGAG-ATCTTCATTGCTCAA</u>
		Type
		CE3 + 3'
		CE2
		PS + CE1
		PS
		PS
		5' + PS
		5'

Coding Interleukin-1 β
IL1B, from cDNA sequence M15330 and genomic sequence X04500.

IL1B-1: \emptyset
IL1B-2: maevpkase mmayys²
IL1B-3: gnehdlifea dgpkqmk³
IL1B-4: csfgldldcp ldggqlris dbhyskgrq aasvvvamd k lrkmlvcpq tfqendlstf fpfifee¹
IL1B-5: piffdtwdnq ayvhdapvis lnctlrdsqg kslvmsgpye lkahlqgqd meqgv¹
IL1B-6: vfsmfsvqge esndkipval alkeknlyls cvlkddkptl ql²
IL1B-7: svdpknypkk kmeqpfvfnk ieinnklefe saqfnpwyis tsqaenmpvf lgytkg99qdl
tdftmqfvss *

FIGURE 18 B

Gene: <i>IL1F7</i>		Orientation: Forward	
Position	Exon	Exon boundaries	Type
204598-204721	<i>IL1F7-b1/c1</i>	<u>CTTCATTC</u> ATTTC-AGTCTGCTTAGA <u>G</u>	5'+PS?
205420-205482	<i>IL1F7-b2/c2</i>	A <u>CCG</u> GCTGGAAGCC-ATTTGTTCA <u>CACAA</u>	PS?
<206821-206887	<i>IL1F7-a1</i>	- <u>ATG</u> TCAGGCTGTGAT-AGAAGCGCTTAAG <u>A</u> G	PS?
208769-208888	<i>IL1F7-a2/b3</i>	<u>GTCCA</u> AGGTGAAGA-ACTACATACG <u>CCCA</u> G	CE1
209275- 209417	<i>IL1F7-a3/b4/c3</i>	AGATCTTCTTTGCAT-TCCCTTCAGCTGA <u>G</u>	CE2
210204- 210529	<i>IL1F7-a4/b5/c4</i>	<u>AAGG</u> AGAACTGATG-AACCTGCTCACTAA	CE3 + 3'
Coding			
Different cDNAs: <i>IL-1F7a</i> (AF201832), <i>IL-1F7b</i> (AF200496) and <i>IL-1F7c</i> (AF251120).			
<i>IL1F7-b1/c1:</i> msfvgensgv kmgse ^d dwkd epqccle ^d <i>IL1F7-b2/c2:</i> pagsplep ^g pg slptmfvht (s/k) ⁱ <i>IL1F7-a1:</i> msgcdrrrete tkgknsfkk ^r lig ^r <i>IL1F7-a2/b3:</i> <u>P</u> kvnl ⁿ pkk fsihdqdhk ^v l ^v ldsgnlia vpdknylrpe ¹ <i>IL1F7-a3/b4/c3:</i> iffalassls sasaekgsp ⁱ llgvs ^k gefc lycdkdkggs hqlk ³ <i>IL1F7-a4/b5/c4:</i> <u>k</u> eklmklaaq kesarrpfif yzaqvgswnm lesaahpgwf ictscncnep vgrtdkfenr khiefsfgpv ckaemsevsd *			

FIGURE 18 C

Gene: <i>IL1F9</i>		Orientation: Forward	
Position	Exon	Exon boundaries	Exon type
269711-269760	<i>IL1F9-1</i>	<u>GAGCCAGATT</u> CAGT-ACCCTTCTTGGCCAG	5'
270302-270375	<i>IL1F9-2</i>	GTGCTGAGACAACCA-CCGCTATCAATCAA	5' + CS
270903-271007	<i>IL1F9-3</i>	TGTGTAAACCTATT-ACAGTGTGACCCGAG	CE1
271691-271830	<i>IL1F9-4</i>	TCACCTGTGCTGTTA-ACATTGCAGCTAAAA	CE2
276523-277335	<i>IL1F9-5</i>	<u>GAGCAGAAGATCATG</u> -CTAAAACTGATATAA	CE3 +3'
Coding			
cDNA sequences AF200492 and AF206696.			
<i>IL1F9-1: Ø</i>			
<i>IL1F9-2: mrgtpgdadg ggravyqsm'</i>			
<i>IL1F9-3: clpiltgtind inqgwtlqg qnlvavprsd svtpv'</i>			
<i>IL1F9-4: tvavitchkyp ealeqgrgdp iylgicnpem clycekygeq ptlqlk'</i>			
<i>IL1F9-5: egkimdlygq pepvksflfy raktgrstl esvafpwwfi asskrdpil ltselgksyn tafelnind*</i>			
Gene: <i>IL1F6</i>		Orientation: Forward	
Position	Exon	Exon boundaries	Exon type
<297556-297565	<i>IL1F6-1?</i>	-ATGGA AAA AG	5' + CS
297658-297771	<i>IL1F6-2</i>	CATTGAAAATTGACA-ACGGTATGTCTCCAG	CE1
298282-298421	<i>IL1F6-3</i>	TCAC TAT TGCCCTTAA-ACACTGCAGCTGAAG	CE2
299516->299728	<i>IL1F6-4</i>	GAAAAGGATATAATG- <u>ACTATGCTGTTTAA...</u>	CE3...
Coding			
cDNA sequences AF201831.			
<i>IL1F6-1: mega'</i>			
<i>IL1F6-2: lkldtpqggs iqdinhrvww lqdtliavp rkdrmspv'</i>			
<i>IL1F6-3: tialiscrhv etlekdrnp iylglinglnl clmcakygdq ptlqlk'</i>			
<i>IL1F6-4: ekdimdlynq pepvksflfy hsqsgnstf esvafpwwfi avsseggcpl iltqelgkan ttdfgltmlf *</i>			

FIGURE 18 D

Gene: <i>IL1F8</i>		Orientation: Reversed	
Positi n	Exon	Exon boundaries	Exon type
<313785-314471	<i>IL1F8-b6</i>	<u>G</u> TAGAAAGAGTGG- <u>T</u> AGTTTTTCCCATGT	CS + 3'
317797-317926	<i>IL1F8-b5</i>	<u>C</u> TTCAGGGCTCCCAA- <u>G</u> GGGAATAGAGTGG	CS
<319597-319809	<i>IL1F8-a5</i>	<u>G</u> AAAAAATATCATG- <u>G</u> ATTCTGTGGAATAA...	CE3...
320633-320772	<i>IL1F8-a4/b4</i>	<u>T</u> CACTCTTCATTAA- <u>A</u> CTTTGCAGCTTAAG	CE2
322742-322849	<i>IL1F8-a3/b3</i>	<u>G</u> GGAGGCAGCACCCA- <u>G</u> CAGCATTAAGCCTG	CE1
323391-323460	<i>IL1F8-a2/b2</i>	<u>C</u> CTCCTCACCACCAT- <u>T</u> CATGAACCCACAAC	5' + CS
344518->344570	<i>IL1F8-a1/b1</i>	<u>G</u> ACACGGGTTCTCC- <u>C</u> TTCACTTTTCTAG...	5'
Coding			
Different cDNAs: <i>IL-1F8a</i> (AF201833), and <i>IL-1F8b</i> (AF200494).			
<i>IL1F8-a1/b1</i> : Ø			
<i>IL1F8-a2/b2</i> : <u>m</u> npgr ¹			
<i>IL1F8-a3/b3</i> : <u>e</u> aapksyair dsrqmwvls gnsllaapls rsikpv ¹			
<i>IL1F8-a4/b4</i> : <u>t</u> lhliacrdt efsdkekgnm vylgikgkdl clfcseiaggk ptlqlk ¹			
<i>IL1F8-a5</i> : <u>e</u> knimdlve kkaqkplff hnkegstsvf qsvsygwf ¹ atsttsqgp ¹ fltkergitn			
ntnfyldsve +			
<i>IL1F8-b5</i> : <u>l</u> qgsqdnigk dtcwklvgh tcinldvres cfmgtdldqwg lqvq ¹			
<i>IL1F8-b6</i> : <u>i</u> kkwkssfqh hhlrkkdkdf smrtnigmp gzm ¹			

FIGURE 18 E

Gene: <i>IL1F5</i>		Orientation: Forward	
<u>Position</u>	<u>Exon</u>	<u>Exon boundaries</u>	<u>Exon type</u>
<350401-350445	<i>IL1F5-b1</i>	..AAGGAGGAGGGAGA-GAAGGAGTGAATAAG	5'
350810-350943	<i>IL1F5-a1</i>	CGCTGGGAATCCTGC-AAGGAACATTCTGAG	5' + SORF
351114-351169	<i>IL1F5-a2/b2</i>	GGGAGTCTACACCCCT-GGCGCTGTGCTTCGG	5' + CS
352555-352640	<i>IL1F5-a3/b3</i>	AATGAAGGACTCGGC-GGAAGGTCATTAAAG	CE1
353827-353954	<i>IL1F5-a4/b4</i>	GTEAAGAGATCAGCG-ACTCTAACACTAGAG	CE2
354156-356451	<i>IL1F5-a5/b5</i>	CCAGTGAACATCATG-AGAAAGAGAAACAAA	CE3 + 3'

Coding:

Different cDNAs: *IL-1F5a* (AF186094 and AJ242737) and *IL-1F5b* (AJ242738).

IL1F5-b1:
IL1F5-a1:
IL1F5-a2/b2:
IL1F5-a3/b3:
IL1F5-a4/b4:
IL1F5-a5/b5:

FIGURE 18 F

Gene: *IL1F10***Orientation: Forward**

<u>Position</u>	<u>Exon</u>	<u>Exon boundaries</u>	<u>Exon type</u>
364023-364475	<i>IL1F10</i> -a1	GGCAGTGGGACTGGG-GGCAAGATACTACAT	5' + CS
366034-366119	<i>IL1F10</i> -a2	AATTAAATATGCAGA-ACAACTGCTGTGCAG	CE1
366244-366555	* <i>IL1F10</i> -b1	GCTGTGGCCTCTCCT-TCCCTACAGCTGGAG	5' + CS + CE2
366428-366555	* <i>IL1F10</i> -a3	AGAAGATCTGCATAC-TCCCTACAGCTGGAG	CE2
366857-367553	<i>IL1F10</i> -a4/b2	GATGTGAACATTGAG-TTATTGTAAACCTCT	CE3 + 3'N

C ding**Different cDNAs: *IL-1F10a* (AF334756) and *IL-1F10b* (AY026753).**

IL1F10-a1: mcslpmaryy i²
IL1F10-a2: ikyadqkaly trdgqllvgd pvadnccae¹
 **IL1F10*-b1: msssfipepl pakslqhgvp lsldsslsll lekicilpnrg
 lartkvpifl giqggsrcla cveteeglql e³
 **IL1F10*-a3: kictlpnrgl drtkvpiflg iqggsrclac veteeglql e³
IL1F10-a4/b2: dvnleelykg geeatrftff qsssgsafrl eaaawpgwfl cgpaepqqpv
 qltkeseart kfyfeqsw*

Gene: *IL1RN (IL1F3)***Orientation: Forward**

<u>Position</u>	<u>Exon</u>	<u>Exon boundaries</u>	<u>Exon type)</u>
409176-409311	<i>IL1RN</i> -b1/c1	GGGCAGCTCCACCCT-TCCCCATGGCTTTAG	5' + CS
411350-411412	<i>IL1RN</i> -c2	CTGACTTGTATGAAG-ATGCTGACTCAAAGG	CS
418888-419017	* <i>IL1RN</i> -a1	GCTGCAGTCACAGAA-GATGCAAGCCTTCAG	5' + SS
418966-419017	* <i>IL1RN</i> -b2/c3	AGACGATCTGCCGAC-GATGCAAGCCTTCAG	CS
420853-420941	<i>IL1RN</i> -a2/b3/c4	AATCTGGGATGTTAA-ATGTCAATTAGAAG	CE1
422321-422433	<i>IL1RN</i> -a3/b4/c5	AAAAGATAGATGTGG-AGACTCCAGCTGGAG	CE2
423932-425290	<i>IL1RN</i> -a4/b5/c6	GCAGTTAACATCACT-AATCTTGAAAATGCC	CE3 + 3'

Coding: Interleukin-1 receptor antagonist**Different cDNAs: pro-sIL-1ra (form a, X52016), lclL-1ra (form b, M55646) and lclL-1raII (form c, X84348).**

IL1RN-b1/c1: mal(e/a)¹
IL1RN-c2: dlyeeggggg gegednadsk e¹
 **IL1RN*-a1: meicrglrsh litlllflfh seticrgrks skmqaf^{r2}
 **IL1RN*-b2/c3: ticrgrks skmqaf^r
IL1RN-a2/b3/c4: iwdvnqktfy lrnnqlvagy lqgpnvnlee¹
IL1RN-a3/b4/c5: kidvvpieph alflgihggk mclscvksqd etrlql e³
IL1RN-a4/b5/c6: avnitdl sen rkqdkrfafi rsdsgpttsf esaacpgwfl ctameadqpv
 sltnmpdegv mvtkfyfqed e*

FIGURE 18 G

Map positions of polymorphic markers

Polymorphism	P sition	Variation (database strand)	Variability	Reference
222/223	069722	[GT]_N	polyallelic	A
<i>IL1A</i>+4845	071555	G/A (SNP)	biallelic	B
<i>gz5/gz6</i>	072250	[AAT]_N	quasi-biallelic	A
<i>IL1A</i>-889	076892	G/A (SNP)	biallelic	A,B
<i>IL1B</i>+3954	124347	A/G (cSNP)	biallelic	A,B
<i>IL1B</i>-511	128822	G/A (SNP)	biallelic	A,B
<i>gaat.p33330</i>	271535	[GAAT]_N	quasi-triallelic	A
<i>Y31</i>	335980	[GT]_N	polyallelic	A
<i>IL1RN</i>+2018	420907	C/T (SNP)	biallelic	B

FIGURE 19